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DDBJRELEASE:AE008898DDBJRELEASESaveLinkLaunchNClustalWPrinter Friendly

LOCUS AE008898 23880 bp DNA linear BCT 31-JUL-2002
 DEFINITION *Salmonella typhimurium* LT2, section 202 of 220 of the complete genome.
 ACCESSION AE008898 AE006468
 VERSION AE008898.1
 KEYWORDS
 SOURCE *Salmonella typhimurium* LT2
 ORGANISM *Salmonella typhimurium* LT2
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Salmonella*.

1 (bases 1 to 23880)

AUTHORS McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W., Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.

TITLE Complete genome sequence of *Salmonella enterica* serovar *Typhimurium* LT2

JOURNAL *Nature* 413 (6858), 852-856 (2001)

MEDLINE 21534948

PUBMED 11677609

2 (bases 1 to 23880)

REFERENCE The *Salmonella typhimurium* Genome Sequencing Project.

AUTHORS Direct Submission

TITLE Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA

JOURNAL COMMENT Supported by NIH grant 5U 01 AI43283

Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs: GLIMMER; <http://www.tigr.org/softlab/glimmer/glimmer.html> and GeneMark; <http://opal.biology.gatech.edu/GeneMark/>

EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; <http://www.genome.ad.jp/kegg/>, and Pedro Romero and Peter Karp at EcoCyc; <http://ecocyc.PangeaSystems.com/ecocyc/>

The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one *m13* subclone.

FEATURES

Location/Qualifiers

source

1..23880
 /organism="Salmonella typhimurium LT2"
 /strain="LT2; SGSC 1412; ATCC 700720"
 /db_xref="ATCC:700720"
 /db_xref="taxon:99287"
 /note="LT2"

gene

107..1036
 /gene="malm"
 /note="synonym: STM4232"

RBS

107..112

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/gene="malM"
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119..1036
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(SW:MALM_SALTY)"
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/protein_id="AAL23056.1"
/db_xref="GI:16422790"
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NKQASVFPAPNVLILDQNMTPSAFPSSYFTYQQPGVMSADRLEGVMRLTPALGQQ
KLYVLVFTTEKDLQQTTTLLDPAKAYAKGVGNSIPIDPDPVARHTTDGVV
KLKVKTNSSSVLVGPLFGSSGTGPVTVGNTAAPVAAPAVAPKKSEPM
LNDESYFNKAIKDAVAKGVDVKALKLDEAERLGSTSARSTFISSVKKGK
1203..1714
/gene="ubiC"
/note="synonym: STM4233"
1203..1208
/gene="ubiC"
/note="putative RBS for ubiC; RegulonDB:STMS1H004138"
1217..1714
/gene="ubiC"
/EC_number="4.-.-.-"
/note="similar to E. coli chorismate lyase (AAC77009.1);
Blastp hit to AAC77009.1 (202 aa), 86% identity in aa 38 -
202"
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/protein_id="AAL23057.1"
/db_xref="GI:16422791"
/translation="MSHPALTQLRALRYFDAIPALEPHLLDWLLLED
SMTKRFEQQGK
RVSVTLIREAFVGQSEVEEASGLPSE
SRYWLRE
I
LLCADGE
PWL
AGRTVV
PESTLCG
PEQVLQHLGKTP
LGRY
LFTS
STL
TRDF
IE
I
GRDATLW
GRRS
RL
LS
GK
P
LL
TE
FLP
ASPLY"
1715..2600
/gene="ubiA"
/note="synonym: STM4234"
1715..1720
/gene="ubiA"
/note="putative RBS for ubiA; RegulonDB:STMS1H004139"
1728..2600
/gene="ubiA"
/EC_number="2.5.1."
/note="similar to E. coli
4-hydroxybenzoate:octaprenyltransferase (AAC77010.1);
Blastp hit to AAC77010.1 (290 aa), 93% identity in aa 1 -
290"
/codon_start=1
/transl_table=11
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/protein_id="AAL23058.1"
/db_xref="GI:16422792"
/translation="MEWSLTQSKLLAFHRLMRTDKP1GALLLWPTLWALWVATPGMP
QLWILAVFVAGVWLMRAAGCVVNDYADRKF
DGHVKRTVNRPLPSGAVTEKEARNLFVV
LVLLAFLLVTLNAMTILSVAALALAWVY
P
FMKRY
L
PQVVLGA
AFGWS
IPMAFAA
VSESLPLSCWLMFLANILWAVAYDTQYAMVDRDDDIKIGIKSTA
L
L
FGRY
DTL
I
IGIL
QLGV
MAL
MAL
I
GWL
NGL
GWG
YY
WAVL
VAG
ALFVY
QQ
QLIAN
R
R
E
A
C
F
K
A
F
M
N
N
Y
VG
L
V
L
F
L
G
L
A
M
S
Y
W
H
F"
complement(2699..5136)
/gene="plsB"
/note="synonym: STM4235"
complement(2699..5119)
/gene="plsB"
/EC_number="2.3.1.15"
/note="similar to E. coli glycerol-3-phosphate
acyltransferase (AAC77011.1); Blastp hit to AAC77011.1
(827 aa), 94% identity in aa 21 - 826"

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/protein_id="AAL23059.1"
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LPYNSKADLLTARAQCLAHLPDPLEPIDEGALLPRYVFHGGPRVFTYTPKEESV
KLFHDYLDLHRSNPALDVQMVVPVSVMFGRAPGREKGEDNPPLRMLNGVQKFFAISWLG
RDSFVRFSPSPSRLRRMADEHGTDK1IAQKLARVARMHFAQRQLAAVGPRLPARQDLFN
KLLASKIAARAVEDEARSKISHEKAQQNAIALMEEIAANFSYEMIRLTDRLGFTWN
RLYQGINVHNAERVRLAHDGHEIVYVPCHRSHMDYLLSYVLYHQGLVPPHIAAGIN
LNFWPAGPIFRRLLGAFFIRRTFKGNKLYSTVRFYLGELFSRGYSVEYFVEGGRRTG
RLLDPKTGTLMSMTIQAMLRGGTRPITLVP1YIGYEHVMEVGTYAKELRGATKEKESLP
QMLKGLSKRLNLGQGYVNFGEPMPLMTYLNQHVPWRESIDPIEAIRPAWLTPTVNSI
AADLMVRINNAGAANAMNLCTALLASRQRSLTREQLTEQLDCYLDLMRNVPYSTDST
VPAASAGELIAHALQMNKFEVEKDITGDIILPREGAVLMTYRRNNIAHMLIMPSLMA
A11TQHRRISRDALQQHVEALYPMKLAELFLRWEREELASVIDALASEMQRQGLITLQ
DDELHINPHTSRTLQLLAAGARETLQRYAITFWLLSANPSINRSTLEKESRTVAQRLS
VLHG1NAPEFFDKAVFSSLVLTLDREGYISDTGDAEPAETMKIYQMLADLITSVRLT
IESATQGE"
RBS
complement(5131..5136)
/gene="plsB"
/note="putative RBS for plsB; RegulonDB:STMS1H004140"
gene
5278..5658
/gene="dgkA"
/note="synonym: STM4236"
RBS
5278..5283
/gene="dgkA"
/note="putative RBS for dgkA; RegulonDB:STMS1H004141"
CDS
5290..5658
/gene="dgkA"
/EC_number="2.7.1.107"
/note="similar to E. coli diacylglycerol kinase
(AAC77012.1); Blastp hit to AAC77012.1 (122 aa), 86%
identity in aa 1 - 121"
/codon_start=1
/transl_table=11
/product="diacylglycerol kinase"
/protein_id="AAL23060.1"
/db_xref="GI:16422794"
/translation="MANNTTGFTRIIKAAGYSWKGFRAAWTHEAAFRQESLAVLLGV
IACWLDVDAITRVLLIGSVLLIMIVEILNSAIEAVVDRIGSEYHELSGRAKDMGSAAV
LLSIFVALMTWKGILLWSHFR"
gene
5701..6375
/gene="lexA"
/note="synonym: STM4237"
5701..5709
/gene="lexA"
/note="putative -35_signal for lexA;
RegulonDB:STMLTH004657"
-35_signal
5722..5738
/gene="lexA"
/note="putative binding site for LexA, RegulonDB:
STMS1H000241"
/bound_moiety="LexA"
5725..5733
/gene="lexA"
/note="putative -10_signal for lexA;
RegulonDB:STMLTH004657"
protein_bind
5742..5762
/gene="lexA"
/note="putative binding site for LexA, RegulonDB:
STMS1H000249"
/bound_moiety="LexA"
-10_signal
5756..5761
/gene="lexA"
/note="putative RBS for lexA; RegulonDB:STMS1H004142"
RBS
5767..6375
/gene="lexA"
/EC_number="3.4.21.88"
/note="transcriptional repressor (LexA family); LEXA"
CDS

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repressor. (SW:LEXA_SALTY)
/codon_start=1
/transl_table=11
/product="SOS response regulator"
/protein_id="AAL23061.1"
/db_xref="GI:16422795"
/translations="MKALTARQEVFDLIRDHISQTGMPPTRAEIAQRLGFRSPNAAE
EHLKALARKGVLIEVSGASRGIRLLQEEEDGLPLVGRVAAGEPLLAQQHIEGHYQVDP
SLFKPSADFLLRVSGMSMKD1G1MDGDLLAVHKTQDVRNGQVVVAR1DDEVTVKRLKK
QGNKVELLPENSEFTPIVVDLREQSFTIEGLAVGVIRNGEWL"

gene 6540..7878
/gene="dinF"
/note="synonym: STM4238"
RBS 6540..6545
/gene="dinF"
/note="putative RBS for dinF; RegulonDB:STMS1H004143"
CDS 6553..7878
/gene="dinF"
/note="induced by UV and mitomycin C; SOS, LexA regulon;
similar to E. coli DNA-damage-inducible protein F
(AAC77014.1); Blastp hit to AAC77014.1 (459 aa), 89%
identity in aa 19 - 457"
/codon_start=1
/transl_table=11
/product="DNA-damage-inducible protein F"
/protein_id="AAL23062.1"
/db_xref="GI:16422796"
/translation="MPLFTSSDKALWRLALPIMFSNITVPLLGVLVDTAVIGHLDSPVF
LGGVAGATATSFMLLFLRMSTTGLTAQAFGAKNPQALARALIQPLLLALGAGVM
IVLFRTPLELALHVCGNDAVLVQARRFLEIRWLSAPASLANLVLLGWLLGVQYARA
PVILLVVGNILNIALDLWLVMLGHMNVQGAALATVIAEYVTLLIGLMMVRKVVLHRCV
SLDMLKQAWRGNVNRLLALNRD1MLRSSLQLCFCGAITVSGARLGSDI1AVNAVLMTL
LTFTAYALDGFAVAYEAHSGQAYGARDGSKLLDVWRAACRQSGIVALLFSTVYALAGE
HIVALLTSLPQIQLLADRYLIWQVVLPLVGVWCYLLGGMFIGATRAAEMRNSMVAAG
GFALTLFALPVVLGNHGLWLAATVFLALRGLSLSIWRRHWREGTWFARS"

gene 7875..7988
/gene="STM4239"
CDS 7875..7988
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/codon_start=1
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/protein_id="AAL23063.1"
/db_xref="GI:16422797"
/translation="MTVKNSEYKTEGRIPAYNYYHVQQKLQSIWANNTCYS"

gene 7998..8219
/gene="yjbJ"
/note="synonym: STM4240"
RBS 7998..8003
/gene="yjbJ"
/note="putative RBS for yjbJ; RegulonDB:STMS1H004144"
CDS 8007..8219
/gene="yjbJ"
/note="similar to E. coli orf, hypothetical protein
(AAC77015.1); Blastp hit to AAC77015.1 (69 aa), 95%
identity in aa 1 - 69"
/codon_start=1
/transl_table=11
/product="putative cytoplasmic protein"
/protein_id="AAL23064.1"
/db_xref="GI:16422798"
/translation="MMNKDEAGGNWKQFKGKMKEQWGKLTDDDMTVIEGKRDQLVGKIQ
QERYGYQKDQAEKEVVWDWETRNNYRW"
complement(8318..8843)
/gene="zur"
/note="synonym: STM4241"
CDS complement(8318..8833)
/gene="zur"
/note="Fur family; similar to E. coli putative regulator
(AAC77016.1); Blastp hit to AAC77016.1 (191 aa), 92%

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identity in aa 21 - 191"
/codon_start=1
/transl_table=11
/product="transcriptional repressor of znuABC operon"
/protein_id="AAL23065.1"
/db_xref="GI:16422799"
/translation="MEKTTTQELLAQAEKLCAQRNVRLTPQRLEVRLMSLQQGAISAYDLDLRETEPQAKPPTIYRALDFLLEQGFVHKVESTNSYVVCFLFDQPTHSSAMFICDRCGVVKEECAEGVEDIMHTLAALKMGFALRHNVIEAHGLCPACVEVEACRHPGNCGHDHSVVKKKPR"
RBS complement(8838..8843)
/gene="zur"
/note="putative RBS for zur; RegulonDB:STMS1H004145"
gene 9076..10390
/gene="STM4242"
RBS 9076..9081
/gene="STM4242"
/note="putative RBS for STM4242; RegulonDB:STMS1H004146"
CDS 9080..10390
/gene="STM4242"
/codon_start=1
/transl_table=11
/product="putative outer membrane or exported protein"
/protein_id="AAL23066.1"
/db_xref="GI:16422800"
/translation="MNKNVKLSSLIAIAVSLFMAKQASAANTWTEARNDAMGGTGVASA
NYGSGVLLNPALLAKAKPEDNTTVVPAVGQITDKDNLQDEIDDSKVDYYDEVVD
NLTLGQILLNPRGVLNQFQGARDLADEELEYLNKTARANAGAGLAWSIPGQTLVAF
IAKGYAHGRVSSSIDQNDIQYLRDIQHDERVALREAGRAALLGSDEITKHLNSTASGR
VAIVSDYGIALAKQFVVGEPVSIGVTPKLQKTLWLYNTTSIYNYDSSDWNSRYRND
DTGFNIDAGLAADIGENWTLGVSGQNLVSRIDTAKDIIYITNGMTGETTNYKDTYQIRP
LVTAGIAWHNDLTVSADGDLTETKGFSKEDNSQYVGVAEVRLPSLWLAVERAGYRADV
KNNDSNVVTGGLGFAPFNRVHLDLMGLYGEDETWGAGAQLTMTF"
gene 10478..11476
/gene="yjbN"
/note="synonym: STM4243"
CDS 10478..11476
/gene="yjbN"
/note="possibly dehydrogenases; nifR3 family; similar to
E. coli orf, hypothetical protein (AAC77019.1); Blastp hit
to AAC77019.1 (345 aa), 90% identity in aa 7 - 345"
/codon_start=1
/transl_table=11
/product="putative TIM-barrel enzyme"
/protein_id="AAL23067.1"
/db_xref="GI:16422801"
/translation="MQPETQSSALPAYRFSIAPMLDWDRHCRYFLRLLSRQTQLYTEMVTTGAIIHGKGDYLAYSEEHPVALQLGGSDPAQLAHCAKLAEARCYDEINLNVCPSDRVQNGMFGACLMGNAQLVADCVKAMRDVVSIPVTVKTRIGIDDDQDSYAFLCDFIDTVSGQGECEMFIIHARKAWLSGLSPKNEIREIPPLDYPRVYQLKRDFPHLTMSINGGIKSLEEAKEHLRHMDGVMVGREAYQNPGLAAVADREIFGADTTDADPVAVVVRAMYPYIERE
LSQGAYLGHITRHMLGLFQGIPGARQWRRYLSENAHKAGADAVAVLEQALKLVADKR"
gene 11631..11886
/gene="yjb0"
/note="synonym: STM4244"
RBS 11631..11636
/gene="yjb0"
/note="putative RBS for yjb0; RegulonDB:STMS1H004147"
CDS 11644..11886
/gene="yjb0"
/note="similar to E. coli orf, hypothetical protein
(AAC77020.1); Blastp hit to AAC77020.1 (150 aa), 82%
identity in aa 71 - 150"
/codon_start=1
/transl_table=11
/product="putative inner membrane protein"
/protein_id="AAL23068.1"
/db_xref="GI:16422802"
/translation="MLELLFVLGFFLMLMVTGVSSLGILAAVAVVATAVMFLGGMFALMIKLLPWLLAVAVVWVVIKAVKTPKIPQYQRNNRRFY"
gene complement(12061..13052)

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/note="synonym: STM4245"
complement(12061..13044)
/CDS
/gene="qor"
/EC_number="1.6.5.5"
/note="similar to E. coli quinone oxidoreductase
(AAC77021.1); Blastp hit to AAC77021.1 (327 aa), 90%
identity in aa 1 - 327"
/codon_start=1
/transl_table=11
/product="NADPH dependent quinone oxidoreductase"
/protein_id="AAL23069.1"
/db_xref="GI:16422803"
/translation="MATRIEFHKHGGPEVLQTVFPTAEPAEHEIQVENKAIGINFI
TYIRSGLYPPPSLPAGLGEAAGVVSKGNGVEHIVGDRVVAQSTLGYSSVHNVT
ADKAAILPDAISFEQAAASFALKGLTVFYLRLKTYEVKDPFLFHAAAGGVGLIACQW
AKALGAKLIGTVGSAQKAQRALDAGAWQVINYREESIVERVKEITGGKKVRRVYDSVG
KDTWEASLDCLQRGGLMSFGNAGPVTGVNLGILNQKGSLYATRPSLQGYITTREEL
TEASNELFLIASGVIVKVDVAENQRYALKDARRAHEVLESRATQGSSLIP"
complement(13047..13052)
/RBS
/gene="qor"
/note="putative RBS for qor; RegulonDB:STMS1H004148"
/gene 13091..14524
/gene="dnab"
/note="synonym: STM4246"
/RBS
13091..13096
/gene="dnab"
/note="putative RBS for dnab; RegulonDB:STMS1H004149"
/CDS
13109..14524
/gene="dnab"
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/note="chromosome replication; chain elongation;
replicative DNA helicase. (SW:DNAB_SALTY)"
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/db_xref="GI:16422804"
/translation="MAGNKPKNPKPQTARDRDPQVAGIKVPPHSIEAEQSVLGMLD
NERWDDVAERVVAEDFYTRPHRHIFTEMGRLQESGSPIDLITLAESLERQGQLDSVGG
FAYLAELSKNTPSAANISAYADIVRERAVVRDMIAVAHEIADAGYDPQGRNSDELLDL
AESRVFQIAENRANKDEGPKSIDQI1DATVARIEQLFQQPHDGVTVGVTGYQDLNKKT
AGLQRSDL11VAARPMSGKTTFAMNLCEAAMLQDKPVLIFSLEMPGEQIMMRMLASL
SRVDQTR1RTGQLDDEDWARISGTMGILLEKRNMYIDSSGLTPTEVRSRARRIFREH
GGLSLIMIDYLQLMRVPSLSDNRTLEIAEISRSLKALAKELQVPVVALSQLNRSLEQR
ADKRPVNSDLRESGSIEQDADLIMF1YRDEVYHENSDLKGIAEIIIGKQRNGPIGTVR
LTFNGQWSRFDNYAGPQYDDE"
/gene 14545..15635
/gene="alr"
/note="synonym: STM4247"
/RBS
14545..14550
/gene="alr"
/note="putative RBS for alr; RegulonDB:STMS1H004150"
/CDS
14556..15635
/gene="alr"
/EC_number="5.1.1.1"
/note="alanine racemase, biosynthetic. (SW:ALR1_SALTY)"
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/transl_table=11
/product="biosynthetic alanine racemase 1"
/protein_id="AAL23071.1"
/db_xref="GI:16422805"
/translation="MQAATVVINRRALRHNLQRLRELAPASKLVAVVKANAYGHGLLE
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EQLAALEAVELAEPVTWMKLDTGMHRLGVRPEEAEAFYQRLTHCKNVRQPVNIVSHF
ARADEPECGATEHQLD1FNAFCQCQKPGQRSLAASGG1LLWPQSHFDWARPG11LYGVS
PLEHKPWGPDFGFPVMSLSSLIAVRDHKAGEPVGYGGTVWSEDRTRLGVVAMGYGD
GYPRAAPSGTPVVLNGREVP1VGRVAMDMICVDLGPNAQDNAGDPVV1WGEGLPVER1
AEMTKVSAYEL1TRLTSRVAMKY1D"
/gene 15773..17014
/gene="tyrB"

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-35_signal      /note="synonym: STM4248"
15773..15781
/gene="tyrB"
/note="putative -35_signal for tyrB;
RegulonDB:STMLTH004658"
protein_bind    15794..15816
/gene="tyrB"
/note="putative binding site for TyrR, RegulonDB:
STMS1H000389"
/bound_moiety="TyrR"
-10_signal      15800..15808
/gene="tyrB"
/note="putative -10_signal for tyrB;
RegulonDB:STMLTH004658"
RBS             15806..15811
/gene="tyrB"
/note="putative RBS for tyrB; RegulonDB:STMS1H004151"
15820..15844
/gene="tyrB"
/note="putative binding site for TyrR, RegulonDB:
STMS1H000384"
/bound_moiety="TyrR"
CDS             15821..17014
/gene="tyrB"
/EC_number="2.6.1.57"
/note="tyrosine repressible; aromatic-amino-acid
aminotransferase. (SW:TYRB_SALTY)"
/codon_start=1
/transl_table=11
/product="tyrosine aminotransferase"
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/db_xref="GI:16422806"
/translation="MFQKVDAYAGDPILSLMERFKDDSRHDKVNLSQLYYNEDGIIIP
QLKTVAAEEARLNAQPHGASLYLPMEGLNTYRHTIAPLLFGADHPVLQQQRVATIQL
GGSGALKVGADFLKRYFPDAGVWVSDPTWENHIAIFAGAGFEVSTYPWYDDATNGIRF
NDLLATLNTLPARSIVLLHPCCCHNPTGADLTPSQWDAVIEIVKARDLIPFLDIAYQGF
GAGMDDDAVYVIRAIASAGLPAVSNSFSKIFSLYGERVGGLSVVCEADEIAARVLGQL
KATVRRIIYSSPPCFGAQVVATVLGDEALKAGWLAEVDAAMRNRIISMRQTLVKEKAE
PDRNFDYLLQQRGMFSYTCSEEQVDRRLRDEFGVYLIASGRMCVAGLNASNVHRVAKA
FAAVM"
gene            17190..17914
/gene="aphA"
/note="synonym: STM4249"
RBS             17190..17195
/gene="aphA"
/note="putative RBS for aphA; RegulonDB:STMS1H004152"
CDS             17201..17914
/gene="aphA"
/EC_number="3.1.3.2"
/note="similar to E. coli diadenosine tetraphosphatase
(AAC77025.1); Blastp hit to AAC77025.1 (237 aa), 89%
identity in aa 1 - 237"
/codon_start=1
/transl_table=11
/product="non-specific acid
phosphatase/phosphotransferase, class B"
/protein_id="AAL23073.1"
/db_xref="GI:16422807"
/translation="MKKITLALSAVCLLFTLNHSANALVSSPSTLNPGTNVAKLAEQA
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